<110> Cahoon, Rebecca
        Gutteridge, Steven
        Lee, Jian-Ming
        McGonigle, Brian
        Rafalski, Antoni

<120> Ornithine Biosynthesis Enzymes

<130> BB-1174

<140> 09/744,100
<141> 2001-01-16

<150> PCT/US99/15931
<151> 1999-07-14

<150> 60/093,209
<151> 1998-07-17

<160> 12

<170> Microsoft Office 97

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<211> 1201
<212> DNA
<213> Zea mays

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tgcaagcccc cttgccgccc ctacttgccg tcgcagccgc ctccgcatct ccgccacatc   180
cacggctgcg ccgtctcctt cgtcggctgc cgctgccacc gcgtcgctga gtcgagtgga   240
cgtgctctcg gaggcgctcc cttttattca gcgattcaaa ggcaagacgg tggtggtcaa   300
gtacggcggt gcggcgatga agtccccgga gctgcaggcg tccgtgatcc gcgatctcgt   360
gctgctctcc tgcgtcggcc tccgccccgt gcttgttcac ggcggcggtc cggagattaa   420
ttcctggctg ctgcgcgtcg gcgtcgagcc gcagttccgc gacggcctcc gcgtcacgga   480
cgcgctcacc atggaggtcg tcgagatggt gctagtcggg aaggtcaaca aaaaccttgt   540
ttccctcatc aacatcgcgg gaggcaccgc cattggtctg tgcggcaagg acgcgcgcct   600
tatcaccgct cgcccgtctc caaatgcagc ggcgctggga ttcgtcggcg aggtttcgcg   660
cgtggacgcc accgtcctcc atcccatcat cgccgcgggc catatcccgg ttatcgccac   720
cgttgccgcc gacgagactg ggcaagccta taacatcaat gctgatacgg cggctggcga   780
gattgccgct gccgtgggcg ccgagaagct gctgttgctc acagatgtgt ctggcatttt   840
ggcggaccgt aatgaccctg ggagcctggt gaaggtggtc gacattgctg gggtgcggaa   900
gatggtggct gacgggaagg tagctggtgg gatgataccc aaggtggagt gttgtgttca   960
cgcccttgca caaggtgtac acaccgcaag tatcattgat gggcgtgttc cacactctct 1020
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atgccttcat ggtatttttcc tgtgcctctt ttctcatatt gttgtgtttt atggctatgt 1140
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<210> 2
<211> 345
<212> PRT
<213> Zea mays

<400> 2
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 1   5   10   15

Ser Pro Pro Pro Ser Gly Pro Thr Leu Ser Ser Asn His Ala Ser Pro
            20   25   30

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Leu Ala Ala Pro Thr Cys Arg Arg Ser Arg Leu Arg Ile Ser Ala Thr
        35              40              45

Ser Thr Ala Ala Pro Ser Pro Ser Ser Ala Ala Ala Ala Thr Ala Ser
        50              55              60

Leu Ser Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg
65              70              75              80

Phe Lys Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys
                85              90              95

Ser Pro Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser
        100             105             110

Cys Val Gly Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile
        115             120             125

Asn Ser Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asp Gly
    130             135             140

Leu Arg Val Thr Asp Ala Leu Thr Met Glu Val Val Glu Met Val Leu
145             150             155             160

Val Gly Lys Val Asn Lys Asn Leu Val Ser Leu Ile Asn Ile Ala Gly
            165             170             175

Gly Thr Ala Ile Gly Leu Cys Gly Lys Asp Ala Arg Leu Ile Thr Ala
            180             185             190

Arg Pro Ser Pro Asn Ala Ala Ala Leu Gly Phe Val Gly Glu Val Ser
        195             200             205

Arg Val Asp Ala Thr Val Leu His Pro Ile Ile Ala Ala Gly His Ile
    210             215             220

Pro Val Ile Ala Thr Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn
225             230             235             240

Ile Asn Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala
            245             250             255

Glu Lys Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg
        260             265             270

Asn Asp Pro Gly Ser Leu Val Lys Val Val Asp Ile Ala Gly Val Arg
        275             280             285

Lys Met Val Ala Asp Gly Lys Val Ala Gly Gly Met Ile Pro Lys Val
    290             295             300

Glu Cys Cys Val His Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile
305             310             315             320

Ile Asp Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp
            325             330             335

Glu Gly Thr Gly Thr Met Ile Thr Gly
            340             345

<210> 3
<211> 1186
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2

<212> DNA
<213> Oryza sativa

<220>
<221> unsure
<222> (613)
<223> n = A, C, G, or T

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ctctttcctc ccatccacgc gggtgtctag ccccgctccg ggtcccaacc acgcaaagcc   120
catcgccgcc tctcccgccc ctcgacgctg cctccgtctc gccgtcacat ccgccgcggc   180
gccggctgct cgtcggcgg aggcggcggc ggcgctgagc cgcgtggatg tgctctcaga   240
ggcgctcccc ttcatccagc gcttcaaggg gaagaccgtg gtggtgaagt acggcggcgc   300
ggcgatgaag tcgccggagc tccaggcttc agtgatccgc gacctggtcc tcctctcgtg   360
cgtcggcctc caccccgtgc tcgtccacgg cggcgggccc gagatcaact cctggctgct   420
ccgcgtcggc gtcgagccgc agttccggaa cggcctccgc gtcactgacg cgctcaacat   480
ggaggtcgtc gagatggtgc tcgtccgcaa ggtcaacaaa gaactcctct ccctcatcaa   540
actcccgggg gggagcgccg taagtctctg ttgaaggaa gctcgcctcc tcaacgagcg   600
gccctcccg aangaaaagg gccttcggtt tgtcggcggg gtctggcgcg tggacgccac   660
cgtcctccac ccaatcatcg cctccggtca catcccggtc atcgccactg tgggcgccga   720
cgagaccggg caggcctaca acatcaacgc tgacacggcg gccggcgaga tcgccgccgc   780
ggtcggcgcg gagaagctgt tgctgctcac agatgtgtct ggaattctgg ccgaccgtaa   840
tgaccccggg agtctggtga aagagatcga cattgctggg gtgcggcaga tggtggccga   900
cgggcaggta gctggtggga tgataccgaa ggtggaatgc tgcgtgcgtg ccctcgcaca   960
gggcgtgcac actgcaagca tcatcgatgg gcgtgtcccg cactcgttgc tgctcgagat  1020
tctcacagat gagggcactg gcactatgat cactggctga ggtgattcat cccgtcgtgg  1080
tattctccgg tgcctctctt ctcatactgt aatgtaattt gcatttgata tgcctcatga  1140
ttgcaataag aattgtattc ctcaaaaaaa aaaaaaaaa aaaaaa             1186
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<210> 4
<211> 343
<212> PRT
<213> Oryza sativa

<220>
<221> UNSURE
<222> (195)
<223> Xaa = ANY AMINO ACID

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  1               5                  10                  15


Thr Arg Val Ser Ser Pro Ala Pro Gly Pro Asn His Ala Lys Pro Ile
            20                  25                  30


Ala Ala Ser Pro Ala Pro Arg Arg Cys Leu Arg Leu Ala Val Thr Ser
        35                  40                  45


Ala Ala Ala Pro Ala Ala Ser Ser Ala Glu Ala Ala Ala Ala Leu Ser
    50                  55                  60


Arg Val Asp Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys
 65                  70                  75                  80


Gly Lys Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro
                85                  90                  95


Glu Leu Gln Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val
            100                 105                 110


Gly Leu His Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser
        115                 120                 125
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3

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Trp Leu Leu Arg Val Gly Val Glu Pro Gln Phe Arg Asn Gly Leu Arg
    130             135             140

Val Thr Asp Ala Leu Asn Met Glu Val Val Glu Met Val Leu Val Arg
145             150             155             160

Lys Val Asn Lys Glu Leu Leu Ser Leu Ile Lys Leu Pro Gly Gly Ser
            165             170             175

Ala Val Ser Leu Cys Trp Lys Glu Ala Arg Leu Leu Asn Glu Arg Pro
        180             185             190

Ser Pro Xaa Glu Lys Gly Leu Arg Phe Val Gly Gly Val Trp Arg Val
        195             200             205

Asp Ala Thr Val Leu His Pro Ile Ile Ala Ser Gly His Ile Pro Val
    210             215             220

Ile Ala Thr Val Gly Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn
225             230             235             240

Ala Asp Thr Ala Ala Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys
        245             250             255

Leu Leu Leu Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp
        260             265             270

Pro Gly Ser Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met
        275             280             285

Val Ala Asp Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys
    290             295             300

Cys Val Arg Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp
305             310             315             320

Gly Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly
            325             330             335

Thr Gly Thr Met Ile Thr Gly
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<211> 1204
<212> DNA
<213> Glycine max

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ccaccgcgcc atttccgcgg tggcgaacgc ggcgcaacct ccactcgccg ccgccactgc   180
caccgagggt cagtaccgag tcgatgtgct ctcggagtcg ctccccttca tccagaaatt   240
ccgcggcaaa accatcgtcg tcaagtacgg cggcgccgcc atgaagtccc cggagctcca   300
ggcctccgtg atcaacgacc ttgtcctcct ctcctgcgtc ggcctccgcc cgtcctggt   360
ccacggcggc ggccccgaga tcaactcctg gctcggccgc ctcaacatcc ccgccgtctt   420
ccgcgacggc ctccgcgtca ccgacgccga caccatggag atcgtctcca tggtcctcgt   480
cggaaaagtc aacaaaaccc tagtttctct aattaacaag gccggcgcca ccgccgtcgg   540
cctctctggc atggacggcc gcctcctcac cgcccgcccc gctcccaagg ccgccgacct   600
cggctacgtc ggcgaggtcg cacgcgtcga tccgccgtc ctccgctccc taatcgacac   660
cagccacatc cccgtcgtca cctccgtcgc cgccgatgaa tccggacagc cctacaacat   720
caacgccgac accgtcgccg gagaattggc agcgtcgctc ggcgcggaga agctgattct   780
gctgaccgat gtggcgggaa ttctggaaga tcggaacgac cctgacagct tggtgaagaa   840
gattgacata aaaggagtga agaaaatgat ggaagatgga aaagttggtg gtggaatgat   900
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4

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acctaaggtt aattgttgcg ttaggtcctt ggcgcaaggg gttattacag cgagtattat  960
tgatggtagg gttccgcatt ctttgttgct tgagattttg actgatgaag gtgctggaac 1020
tatgataact ggataagttt atttatttat ggtgtttgga ttttttcttt tcaatcaagc 1080
cttgagttga ggttgcattg cagcacttgt tttgttagag attggtgatt gtttttaagt 1140
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aaaa                                                               1204

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<211> 342
<212> PRT
<213> Glycine max

<400> 6
Met Met Ala Gly Ala Ala Lys Thr Leu Thr Asn Leu Cys Pro Ser Phe
  1               5                  10                  15

Pro Phe Pro Thr Lys Pro Gln Asn Gln Leu Thr Thr Ser His Ala Phe
             20                  25                  30

Pro Ser Thr Arg Leu Arg His Arg Ala Ile Ser Ala Val Ala Asn Ala
             35                  40                  45

Ala Gln Pro Pro Leu Ala Ala Ala Thr Ala Thr Glu Gly Gln Tyr Arg
         50                  55                  60

Val Asp Val Leu Ser Glu Ser Leu Pro Phe Ile Gln Lys Phe Arg Gly
 65                  70                  75                  80

Lys Thr Ile Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu
                 85                  90                 .95

Leu Gln Ala Ser Val Ile Asn Asp Leu Val Leu Leu Ser Cys Val Gly
             100                 105                 110

Leu Arg Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp
             115                 120                 125

Leu Gly Arg Leu Asn Ile Pro Ala Val Phe Arg Asp Gly Leu Arg Val
         130                 135                 140

Thr Asp Ala Asp Thr Met Glu Ile Val Ser Met Val Leu Val Gly Lys
145                 150                 155                 160

Val Asn Lys Thr Leu Val Ser Leu Ile Asn Lys Ala Gly Ala Thr Ala
                 165                 170                 175

Val Gly Leu Ser Gly Met Asp Gly Arg Leu Leu Thr Ala Arg Pro Ala
             180                 185                 190

Pro Lys Ala Ala Asp Leu Gly Tyr Val Gly Glu Val Ala Arg Val Asp
         195                 200                 205

Pro Ala Val Leu Arg Ser Leu Ile Asp Thr Ser His Ile Pro Val Val
210                 215                 220

Thr Ser Val Ala Ala Asp Glu Ser Gly Gln Pro Tyr Asn Ile Asn Ala
225                 230                 235                 240

Asp Thr Val Ala Gly Glu Leu Ala Ala Ser Leu Gly Ala Glu Lys Leu
                 245                 250                 255

Ile Leu Leu Thr Asp Val Ala Gly Ile Leu Glu Asp Arg Asn Asp Pro
             260                 265                 270
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5

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Asp Ser Leu Val Lys Lys Ile Asp Ile Lys Gly Val Lys Lys Met Met
        275                 280                 285

Glu Asp Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Asn Cys Cys
        290                 295                 300

Val Arg Ser Leu Ala Gln Gly Val Ile Thr Ala Ser Ile Ile Asp Gly
305                 310                 315                 320

Arg Val Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Ala
                325                 330                 335

Gly Thr Met Ile Thr Gly
            340


<210> 7
<211> 1246
<212> DNA
<213> Triticum aestivum

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<221> unsure
<222> (492)..(542)
<223> n = A, C, G, or T

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ctaacctaaa ggccgcccgc gtcaggcccc tcgcctcctc cgcgccccat ggacgccgcg  180
ggctccgcgt ctcggcctcc tcctcctccc tggcgccagc gcaggccgcg tccgcggcgc  240
tgaaccgcgt ggacgtcctg tcggaggcgc tccccttcat ccagcggttc aagggcaaga  300
cggtggtggt caagtacggc ggcgcggcca tgaagtcgcc ggagctgcag gcgtcggtga  360
tccgcgacct ggtcctcctc tcctgcgtcg gcctgcgccc cgtgctcgtg cacggcggcg  420
gcccggagat caactcctgg ctgcagcgcg tcggggtcta gccgcagttc cgcaacggcc  480
tccgcgtcac gnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  540
nnaagcagct cttatcccta atcaggcctg cggggaccac agcagttggc ctctgcagaa  600
aggacgggcg catcctaacg gagcgcccct ccccagacgc cgcagccctc gggttcgtcg  660
gcgaggtcac gagaaaaaac ccctctgtgc tccacccgat catcgcctcc agccacatcc  720
cggtcatcgc caccgtggct gccgacgaga ccgggcaagc ctataacatc aacgctgaca  780
ctgcggcggg ggagatcgcg gctgccattg gcgccgagaa gctgttgctg atcactgacg  840
tgtccggcat actcgcggac cgggatgacc ccgggagcct ggtgaaggag attgacatcg  900
ccggcgtacg gcggatggtg gccgagggca aggtgggtgg gggcatgata cccaaggtgg  960
ggtgctgcgt gcgcgcgctg gcgcagggcg tgcacacggc cagcatcatt gacggccgcg 1020
tcccgcactc tctcctgctc gaaatcctca ccgacgaggg caccggcacc atgatcaccg 1080
gctgaaactt gtttgtttgt tgttgttttt ttcttttctt ttttggttca cattctttgg 1140
gttggatggt tttgcatccc tcatttgtgt taaatgtgtt ttcgattcga atcctgaaca 1200
aggagtggtg aaagattgca gctttaagca aaaaaaaaaa aaaaaa           1246

<210> 8
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<212> PRT
<213> Triticum aestivum

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<222> (133)
<223> Xaa = ANY AMINO ACID

<220>
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<222> (144)..(160)
<223> Xaa = ANY AMINO ACID
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<400> 8

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Leu Pro Asn Pro Asn Leu Lys Ala Ala Arg Val Arg Pro Leu Ala Ser
                20   25   30

Ser Ala Pro His Gly Arg Arg Gly Leu Arg Val Ser Ala Ser Ser Ser
            35   40   45

Ser Leu Ala Pro Ala Gln Ala Ala Ser Ala Ala Leu Asn Arg Val Asp
        50   55   60

Val Leu Ser Glu Ala Leu Pro Phe Ile Gln Arg Phe Lys Gly Lys Thr
65   70   75   80

Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Ser Pro Glu Leu Gln
                85   90   95

Ala Ser Val Ile Arg Asp Leu Val Leu Leu Ser Cys Val Gly Leu Arg
            100   105   110

Pro Val Leu Val His Gly Gly Gly Pro Glu Ile Asn Ser Trp Leu Gln
        115   120   125

Arg Val Gly Val Xaa Pro Gln Phe Arg Asn Gly Leu Arg Val Thr Xaa
    130   135   140

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
145   150   155   160

Lys Gln Leu Leu Ser Leu Ile Arg Pro Ala Gly Thr Thr Ala Val Gly
                165   170   175

Leu Cys Arg Lys Asp Gly Arg Ile Leu Thr Glu Arg Pro Ser Pro Asp
        180   185   190

Ala Ala Ala Leu Gly Phe Val Gly Glu Val Thr Arg Lys Asn Pro Ser
        195   200   205

Val Leu His Pro Ile Ile Ala Ser Ser His Ile Pro Val Ile Ala Thr
    210   215   220

Val Ala Ala Asp Glu Thr Gly Gln Ala Tyr Asn Ile Asn Ala Asp Thr
225   230   235   240

Ala Ala Gly Glu Ile Ala Ala Ala Ile Gly Ala Glu Lys Leu Leu Leu
            245   250   255

Ile Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asp Asp Pro Gly Ser
        260   265   270

Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Arg Met Val Ala Glu
        275   280   285

Gly Lys Val Gly Gly Gly Met Ile Pro Lys Val Gly Cys Cys Val Arg
    290   295   300

Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
305   310   315   320

Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
            325   330   335

7

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Met Ile Thr Gly
            340


<210> 9
<211> 439
<212> DNA
<213> Triticum aestivum

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ggggtgcggc agatggtatc cggtgggcag gttgctggtg gaatgatccc aaaggtggag  180
tgctgcgtga gagccctcgc ccagggtgtg cacactgcaa gcatcatcga tgggcgtgtc  240
ccgcactcgc tgttgctcga gattctcaca gatgagggca ctggcacaat gatcaccggc  300
taaggtgtaa aatgcctcct tggtacttcc ttatgccttt ctgttcatac tgccaatctg  360
ccatgtaatt tatgccaatg tagcctcacc tcatgattgc aataagagta ccttcctgac  420
aaaaaaaaaa aaaaaaaaa                                                439


<210> 10
<211> 100
<212> PRT
<213> Triticum aestivum

<400> 10
Ala Arg Gly Glu Ile Ala Ala Ala Val Gly Ala Glu Lys Leu Leu Leu
 1               5                  10                  15

Leu Thr Asp Val Ser Gly Ile Leu Ala Asp Arg Asn Asp Pro Gly Ser
            20                  25                  30

Leu Val Lys Glu Ile Asp Ile Ala Gly Val Arg Gln Met Val Ser Gly
        35                  40                  45

Gly Gln Val Ala Gly Gly Met Ile Pro Lys Val Glu Cys Cys Val Arg
    50                  55                  60

Ala Leu Ala Gln Gly Val His Thr Ala Ser Ile Ile Asp Gly Arg Val
65                  70                  75                  80

Pro His Ser Leu Leu Leu Glu Ile Leu Thr Asp Glu Gly Thr Gly Thr
                85                  90                  95

Met Ile Thr Gly
            100


<210> 11
<211> 297
<212> PRT
<213> Synechocystis sp.

<400> 11
Met Ser Ser Thr Gln Asp Tyr Ile Gly Glu Glu Ala Ala Thr Arg Val
 1               5                  10                  15

Lys Ile Leu Ser Glu Ala Leu Pro Tyr Ile Gln His Phe Ala Gly Arg
            20                  25                  30

Thr Val Val Val Lys Tyr Gly Gly Ala Ala Met Lys Asp Ser Asn Leu
        35                  40                  45

Lys Asp Lys Val Ile Arg Asp Ile Val Phe Met Ala Ser Val Gly Ile
    50                  55                  60
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8

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Arg Pro Val Val Val His Gly Gly Gly Pro Glu Ile Asn Thr Trp Leu
 65             70             75             80

Asp Lys Val Gly Ile Glu Pro Gln Phe Lys Asp Gly Leu Arg Val Thr
             85             90             95

Asp Ala Ala Thr Met Asp Ile Val Glu Met Val Leu Val Gly Arg Val
         100             105             110

Asn Lys Glu Leu Val Asn Leu Ile Asn Gln Ala Gly Gly Lys Ala Val
         115             120             125

Gly Leu Cys Gly Lys Asp Gly Gln Leu Met Thr Ala Arg Thr Met Thr
     130             135             140

Asn Lys Asp Val Gly Phe Val Gly Glu Val Ser Ser Val Asp Ala Arg
145             150             155             160

Val Val Glu Thr Leu Val Lys Ser Gly Tyr Ile Pro Val Ile Ser Ser
             165             170             175

Val Ala Ala Asp Glu Phe Gly Gln Ala His Asn Ile Asn Ala Asp Thr
         180             185             190

Cys Ala Gly Glu Leu Ala Ala Ala Leu Gly Ala Glu Lys Leu Ile Leu
     195             200             205

Leu Thr Asp Thr Arg Gly Ile Leu Arg Asp Tyr Lys Asp Pro Ser Thr
     210             215             220

Leu Ile His Lys Leu Asp Ile Gln Gln Ala Arg Glu Leu Ile Gly Ser
225             230             235             240

Gly Ile Val Ala Gly Gly Met Ile Pro Lys Val Thr Cys Cys Val Arg
             245             250             255

Ser Leu Ala Gln Gly Val Arg Ala Ala His Ile Leu Asp Gly Arg Leu
         260             265             270

Pro His Ala Leu Leu Leu Glu Val Phe Thr Asp Leu Gly Ile Gly Ser
     275             280             285

Met Ile Val Ala Ser Gly Tyr Asp Leu
    290             295


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<211> 346
<212> PRT
<213> Artificial Sequence

<220>
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<222> (2)
<223> Xaa = Leu OR Met

<220>
<221> UNSURE
<222> (3)
<223> Xaa = Leu OR Ala
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9

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<222> (4)
<223> Xaa =  Thr, Ala, OR Gly


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<222> (5)
<223> Xaa = Lys OR NONE


<220>
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<222> (6)
<223> Xaa = Pro OR NONE


<220>
<221> UNSURE
<222> (7)
<223> Xaa = His, Tyr, OR NONE


<220>
<221> UNSURE
<222> (8)
<223> Xaa = Leu OR NONE


<220>
<221> UNSURE
<222> (9)
<223> Xaa = Ser, Ala, OR NONE


<220>
<221> UNSURE
<222> (10)
<223> Xaa = Asn, Ser, Ala, OR NONE


<220>
<221> UNSURE
<222> (11)
<223> Xaa = Ser, Lys, OR Pro


<220>
<221> UNSURE
<222> (12)
<223> Xaa = Leu, Ser, Thr, OR Ala


<220>
<221> UNSURE
<222> (13)
<223> Xaa = Leu OR Phe


<220>
<221> UNSURE
<222> (14)
<223> Xaa = Pro, Thr, OR NONE


<220>
<221> UNSURE
<222> (15)
<223> Xaa = Val, Leu, OR Asn


<220>
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<222> (16)
<223> Xaa = Pro OR Leu
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<220>
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<222> (17)
<223> Xaa = Ser OR Cys

<220>
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<222> (18)
<223> Xaa = Pro, Thr, OR Ala

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<222> (19)
<223> Xaa = Pro, Arg, OR Ser

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<222> (20)
<223> Xaa = Pro, Val, Phe, OR Leu

<220>
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Lys Ser Pro Glu Leu Gln Ala Ser Val Ile Xaa Asp Leu Val Leu Leu
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Ser Cys Val Gly Leu Xaa Pro Val Leu Val His Gly Gly Gly Pro Glu
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Ile Asn Ser Trp Leu Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Phe Arg Xaa
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Gly Leu Arg Val Thr Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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